

STIC-Biotech/ChemLib

165712

From: Bowman, Amy
Sent: Wednesday, September 14, 2005 2:24 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/738,413

Hello,
I need SEQ ID NO: 1 in application 10/738,413 searched, length limited to 21 nucleotides.
Thank you,
Amy Bowman
AU 1635
mail REM 2C18
REM 2C31
571-272-0755

CRPG

EDWARD HART

9/19/05

9/15/05

1-NA
01

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art found, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not** found:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop-off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:08:30 ; Search time 1540 Seconds

(without alignments)
660.753 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uagagaccgcagcagucucut 21

Scoring table: IDENTITY_NUC

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	62.9	19	4	DOG20402
2	12.8	61.0	20	6	AR12581
3	12.8	61.0	21	6	BD171375
4	12.8	61.0	21	6	BD173609
5	12.4	59.0	19	12	AB069169
6	12.4	59.0	20	6	AR315617
7	12.4	59.0	20	6	AX462804
8	12.2	58.1	20	6	AR257223
9	12.2	58.1	20	6	AR259493
10	12	57.1	17	6	AX264519
11	12	57.1	17	6	AX264520
12	12	57.1	17	6	AX264523
13	12	57.1	17	6	AX264524
14	12	57.1	17	6	AX687762
15	12	57.1	17	6	AX687763
16	12	57.1	17	6	AX687764
17	12	57.1	17	6	AX687765
18	12	57.1	17	6	AX687766
19	12	57.1	17	6	AX687767

20	12	57.1	20	6	AX62811	AX62811 Sequence
21	12	57.1	21	6	AR123316	AR123316 Sequence
22	12	57.1	21	6	AR487412	AR487412 Sequence
23	12	57.1	21	6	AR529674	AR529674 Sequence
24	12	57.1	21	6	AX095699	AX095699 Sequence
25	11.8	56.2	17	6	AX726633	AX726633 Sequence
26	11.8	56.2	17	6	AX757199	AX757199 Sequence
27	11.8	56.2	20	6	CQ873538	CQ873538 Sequence
28	11.8	56.2	20	6	AR221414	AR221414 Sequence
29	11.8	56.2	20	6	AR230996	AR230996 Sequence
30	11.8	56.2	20	6	AR271825	AR271825 Sequence
31	11.8	56.2	20	6	AR477925	AR477925 Sequence
32	11.8	56.2	21	6	AR530156	AR530156 Sequence
33	11.8	56.2	21	6	AX096181	AX096181 Sequence
34	11.6	55.2	20	6	AR067013	AR067013 Sequence
35	11.6	55.2	20	6	AR150409	AR150409 Sequence
36	11.6	55.2	20	6	BD228282	BD228282 Antisense
37	11.6	55.2	20	6	AR231077	AR231077 Sequence
38	11.6	55.2	20	6	AR312358	AR312358 Sequence
39	11.6	55.2	20	6	AX378632	AX378632 Sequence
40	11.4	54.3	13	6	E14819	E14819 PCR primer
41	11.4	54.3	16	6	AX255813	AX255813 Sequence
42	11.4	54.3	17	6	I26890	I26890 Sequence 11
43	11.4	54.3	17	6	I91631	I91631 Sequence 11
44	11.4	54.3	17	6	AR286107	AR286107 Sequence
45	11.4	54.3	17	6	AR286487	AR286487 Sequence

ALIGNMENTS

RESULT 1
LOCUS DOG20402 19 bp DNA linear MAM 11-JUN-1993
DEFINITION Dog (Clone: CXK.204) primer for STS 204, 3' end.

VERSION L15665.1 GI:290145
KEYWORDS PCR identification; PCR primer; STS.

SEGMENT 2 of 2
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

| AUTHORS Ostrander,E.A., Sprague,G.F., Jr. and Rine,J.D. |
| TITLE Identification and characterization of dinucleotide repeat (CA)n markers for genetic mapping in dog |
| Genomics (1993) In press |
| Original source text: Canis familiaris (library: E. Ostrander, in pBluescript+) adult spleen DNA. |
| Submitted by: Human Genome Center, |
| Lawrence Berkeley Laboratory, |
| 1 Cyclotron Road, Berkeley, CA 94720, USA |
| e-mail: EOstrander@lbl.gov |
| PCR Buffer: PCR buffer (Perkin-Elmer/Cetus) |
| PCR Profile: Denaturation: 94 degrees C for 1.00 minute |
| Annealing: 55 or 59 degrees C for 0.45 minutes |
| Polymerization: 74 degrees C for 1.00 minutes |
| PCR Cycles: 33 |
| Final Extension: 74 degrees C for 5.00 minutes. |
| Location/Qualifiers |
| 1..19 |
| /organism="Canis familiaris" |
| /mol_type="genomic DNA" |
| /db_xref="taxon:9615" |
| /tissue_type="spleen" |
| /dev_stage="adult" |
| /tissue_lib="E. Ostrander, in pBluescript+" |
| complement(1..19) |
| /evidence=experimental |

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Query Match 62.9%; Score 13.2; DB 4; Length 19;

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Best Local Similarity 72.2%; Pred. NO. 2.4e+04;
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Oy 4 GACCGCCAGGUCUUTT 21
    ||||| |||
Db 19 GACCTGCCAGCACTTT 2

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RESULT 2			
LOCUS	AR125581		
DEFINITION	AR125581	20 bp	DNA
ACCESSION	Sequence 82 from patent US 6177273.		linear
VERSION	AR125581		PAT 16-MAY-2001
KEYWORDS	AR125581.1 GI:14111643		
SOURCE	.		
ORGANISM	Unknown.		
	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 20)		
TITLE	Bennett,C.Frank. and Cowser,L.M.		
JOURNAL	Antisense modulation of integrin-linked kinase expression		
FEATURES	Patent: US 6177273-A 82 23-JAN-2001;		
	Location/Qualifiers		
source	1..20		

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/mmol_type="unassigned DNA
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Query Match	61.0%	Score 12.8	DB 6	Length 20
Best Local Similarity	68.8%	Pred. No. 4.2e+04		
Matches 11, Conservative	3	Mismatches 2	Indels 0	Gaps 0

QY	2	AGGACCGCCAGUGC	17
		: :	
Db	3	AGGACCTTCAGTCCT	18

RESULT 3			
BD171375			
LOCUS	21 bp	DNA	linear
DEFINITION	Method for detecting bronchial asthma risk factor.		
	BD171375		PAT 18-FEB-2003

ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences. 1 (bases 1 to 21)
AUTHORS	Nakamura,Y. and Tamari,M.
TITLE	Method for detecting bronchial asthma risk factor
JOURNAL	Patent: JP 2002218997-A 10 06-AUG-2002;

COMMENT OS Artificial Sequence
PN JP 2002218997-A/10

```

PF 25-JAN-2001 JP 2001017076
PI YUSUKE NAKAMURA MAYUMI TAMARI
PC C12Q1/68.C12N15/09.C12N15/00
CC Primer sequence (F5) for PCR
CM key Location/Qualifiers
FH source
FT 1..21
    Location/Qualifiers
    1..21
FEATURES
    source
    1..21

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ORIGIN

Query Match	61.0%	Score 12.8;	DB 6;	Length 21;
Best Local Similarity	62.5%	Pred. No. 4.2e+04;		
Matches 10; Conservative	4;	Mismatches 2;	Indels 0;	Gaps 0;

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Qy      5 ACCUGCCAGUGCUCU 20
         |||:|||||: : :|
Db      5 ACCTGCCAGTGT 20
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RESULT 4	
BD173609	
LOCUS	BD173609 21 bp DNA linear PAT 18-FEB-2003
DEFINITION	Method of detecting bronchial asthma onset risk factor.
ACCESSION	BD173609
VERSION	BD173609.1 GI:28414940
KEYWORDS	WO 02059305-A/10.
SOURCE	synthetic construct
ORGANISM	synthetic construct
	other sequences; artificial sequences.

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 21)	Nakamura, Y. and Tamari, M.	Method of detecting bronchial asthma onset risk factor	Patent: WO 02059305-A 10 01-AUG-2002;

OTSUKA PHARMACEUTICAL CO LTD, YUSUKE NAKAMURA, MAYUMI TAMARI
OS Artificial Sequence

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PF 25-JAN-2002 WO 2002JP000540
PI 25-JAN-2001 JP OIP 017076
PR YUSUKE NAKAMURA, MAYUMI TAMAYA
PC C12N15/12, C12Q1/68, G01N33/5C
CC Primer sequence (F5) for PC
FH
FT source location/Qu
1. 21
/organism='
FT
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source      location/Qualifiers
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Query Match	61.0%	Score 12.8;	DB 6;	Length 21;
Best Local Similarity	62.5%	Pred. No. 4.2e+04;		
Matches 10; Conservative	4;	Mismatches 2;	Indels 0;	Gaps 0;

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QY      5 ACCUGCCAGUCUCU  20
         |||:|||||:| : :|
Db      5 ACCTGCCAGTGT  20

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RESULT 5	LOCUS	DEFINITION	AB069169	19 bp	DNA	linear	SYN 21-MAY-2003
AB069169			Synthetic construct DNA, reverse primer for human STS sts-R-100A7R at 1p36.				
ACCESSION			AB069169				
VERSION			AB069169.1				GI:15129973

SOURCE ORGANISM	synthetic construct synthetic construct other sequences; artificial sequences
-----------------	---

AUTHORS
Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.

TITLE A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)

REFERENCE	2 (bases 1 to 19)
POBMEB	113 / 4502

REFERENCE	AUTHORS	TITLE	JOURNAL
2 (Vols 1 to 15)	Hori, A.	Direct Submission	Submitted (04-AUG-2001)
			Akira Hori, Tohoku University School of

Miyagi 980-8575, Japan (E-mail:horie@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)

FEATURES

source

Location/Qualifiers

1..19

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

misc_feature

1..19
/note="reverse primer for human STS sts-R-100A7R at 1p36
sts-R-100A7R obtained from clones B100A7, Human BAC
library RPCI-11"

ORIGIN

Query Match 59.0%; Score 12.4; DB 12; Length 19;
Best Local Similarity 85.7%; Pred. No. 7.1e+04;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGACCGCCAGUG 15
DB 3 AGACCTGCCAGAG 16

RESULT 6

LOCUS AR315617/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6154 from patent US 6559294.
ACCESSION AR315617
VERSION AR315617.1 GI:31709043

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Holseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6154 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 64.3%; Pred. No. 7.1e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 UGCCAGUCGUCUT 21
DB 15 TGCTGTGCTCTTT 2

RESULT 7

LOCUS AX462804/c 20 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 548 from Patent EP1217079.
ACCESSION AX462804
VERSION AX462804.1 GI:21886030

KEYWORDS
SOURCE Aegilops tauschii
ORGANISM Aegilops tauschii

REFERENCE 1
AUTHORS Bernard,M., Sourdilile,P. and Guyomarch,H.
TITLE Microsatellite markers from Triticum tauschii
JOURNAL Patent: EP 1217079-A 548 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="Aegilops tauschii"
/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:37682"

Query Match 59.0%; Score 12.4; DB 6; Length 20;
Best Local Similarity 78.6%; Pred. No. 7.1e+04;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGACCGCCAGUG 15
DB 18 AGACCTGCCATTG 5

RESULT 8

LOCUS AR257223/c 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 78 from patent US 6485974.
ACCESSION AR257223
VERSION AR257223.1 GI:27307007

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Popoff,I.
TITLE Antisense modulation of PTPN2 expression
JOURNAL Patent: US 6485974-A 78 26-NOV-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 20;
Best Local Similarity 58.8%; Pred. No. 9.3e+04;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAGACCGCCAGUCU 17
DB 20 TAGTAACTGACAGTCT 4

RESULT 9

LOCUS AX294943 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 6705 from Patent WO0179548.
ACCESSION AX294943
VERSION AX294943.1 GI:17056626

KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany,F., Zivri,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL Sequence differences using ligase detection reaction
PATENT: WO 0179548-A 6705 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical probe sequence"

ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 20;
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Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 GACCGCCAGUCUCUT 20
DB 4 GACCTCCCGGCGCTT 20

RESULT 10
AX264519/c
LOCUS AX264519 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1910 from Patent WO0173002.
ACCESSION AX264519
VERSION AX264519.1 GI:16513318
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Kmiec, E.B., Gamper, H.B. and Rice, M.C.
JOURNAL Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 1910 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Best Local Similarity 91.7%; Pred. No. 1.2e+05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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16 AGGACCTGCCAG 5
Db

RESULT 11
AX264520
LOCUS AX264520 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1911 from Patent WO0173002.
ACCESSION AX264520
VERSION AX264520.1 GI:16513319
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Kmiec, E.B., Gamper, H.B. and Rice, M.C.
JOURNAL Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 1911 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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2 AGGACCTGCCAG 13
Db

RESULT 12
AX264523/c
LOCUS AX264523 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1914 from Patent WO0173002.
ACCESSION AX264523
VERSION AX264523.1 GI:16513322

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Kmiec, E.B., Gamper, H.B. and Rice, M.C.
JOURNAL Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 1914 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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|||||:
12 AGGACCTGCCAG 1
Db

RESULT 13
AX264524
LOCUS AX264524 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1915 from Patent WO0173002.
ACCESSION AX264524
VERSION AX264524.1 GI:16513323
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1
TITLE Kmiec, E.B., Gamper, H.B. and Rice, M.C.
JOURNAL Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 1915 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Best Local Similarity 91.7%; Pred. No. 1.2e+05;
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QY 2 AGGACCTGCCAG 13
|||||:
6 AGGACCTGCCAG 17
Db

RESULT 14
AX687762/c
LOCUS AX687762 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 494 from Patent EP1281758.
ACCESSION AX687762
VERSION AX687762.1 GI:29410458
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1
Shannon, M., Gu, Y. and Nguyen, C.T.

TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

JOURNAL mdz12 Patent: EP 1281758-A 494 05-FEB-2003;

FEATURES Aeomica, Inc. (US)

source Location/Qualifiers

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 75.0%; Pred. No. 1.2e+05; Mismatches 0; Gaps 0;

Matches 9; Conservative 3; Indels 0;

QY 10 CCAGUGCUCCTT 21

Db 17 CCAGTGTCTCTT 6

RESULT 15

AX687763/c 17 bp DNA linear PAT 31-MAR-2003

LOCUS Sequence 495 from Patent EP1281758.

DEFINITION AX687763

ACCESSION AX687763.1 GI:29410459

VERSION AX687763.1 GI:29410459

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Shannon, M., Gu, Y. and Nguyen, C.T.

AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

TITLE mdz12

JOURNAL Patent: EP 1281758-A 495 05-FEB-2003;

FEATURES Aeomica, Inc. (US)

source Location/Qualifiers

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ORIGIN /db_xref="taxon:9606"

Query Match 57.1%; Score 12; DB 6; Length 17;

Best Local Similarity 75.0%; Pred. No. 1.2e+05;

Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 16 CCAGTGTCTCTT 5

Search completed: September 17, 2005, 10:47:56

Job time : 1546 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:06:56; Search time 256 Seconds
(without alignments)
485,604 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uagaccugccagugcucut 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2380332

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	15	71.4	20 4	AA166582
C 2	13.6	64.8	20 12	ADP68070
C 3	13.6	64.8	20 12	ADP68033
C 4	13.2	62.9	20 12	ADH64423
C 5	13.2	62.9	20 12	ADH64554
C 6	13.2	62.9	20 12	ADH63908
C 7	12.8	61.0	17 11	ADL48810
C 8	12.8	61.0	17 11	ADL48391
C 9	12.8	61.0	19 12	ADL14399
C 10	12.8	61.0	20 4	AA166953
C 11	12.8	61.0	20 10	ADP64705
C 12	12.8	61.0	20 10	ADH54183
C 13	12.8	61.0	20 12	ADH54183
C 14	12.8	61.0	20 12	ADH63823
C 15	12.8	61.0	20 12	ADH63823
C 16	12.8	61.0	20 12	ADH63823
C 17	12.8	61.0	20 12	ADH63823
C 18	12.8	61.0	20 12	ADH63823
C 19	12.8	61.0	20 12	ADH63823
C 20	12.8	61.0	20 12	ADH63823

C 21	12.8	61.0	20 12	ADM15205	ADM15205 Human mpg
C 22	12.8	61.0	20 12	ADM14808	ADM14808 Human mpg
C 23	12.8	61.0	21 6	AA144199	AA144199 Human I-X
C 24	12.6	60.0	19 4	AA695089	AA695089 Human oto
C 25	12.6	60.0	20 2	AAV65046	AAV65046 M. pneumo
C 26	12.6	60.0	20 3	AAAI4197	AAAI4197 M. pneumo
C 27	12.6	60.0	20 10	AB285113	AB285113 Human oli
C 28	12.6	60.0	20 11	ABD21343	ABD21343 Human tra
C 29	12.6	60.0	21 9	ABD58127	ABD58127 GAPDH bpe
C 30	12.6	60.0	21 10	ADDA4397	ADDA4397 Rat GAPDH
C 31	12.4	59.0	17 2	AAV95322	AAV95322 Human c-f
C 32	12.4	59.0	18 12	ADK15803	ADK15803 Human ABC
C 33	12.4	59.0	20 2	AA205318	AA205318 PCR prime
C 34	12.4	59.0	20 2	AA296828	AA296828 PCR prime
C 35	12.4	59.0	20 6	ABQ93280	ABQ93280 T. cauch
C 36	12.4	59.0	20 6	AB660954	AB660954 Human gen
C 37	12.4	59.0	20 12	ADN14770	ADN14770 Human mpg
C 38	12.4	59.0	20 12	ADN15365	ADN15365 Human VEG
C 39	12.4	59.0	20 12	ADN94834	ADN94834 Human nid
C 40	12.2	58.1	19 10	ADP37557	ADP37557 Human VEG
C 41	12.2	58.1	19 10	ADP37310	ADP37310 Human VEG
C 42	12.2	58.1	19 12	ADQ60823	ADQ60823 Ant1-IRS1
C 43	12.2	58.1	20 6	AB194985	AB194985 Capture o
C 44	12.2	58.1	20 8	AAD53632	AAD53632 Human ptp
C 45	12.2	58.1	20 10	ADP88187	ADP88187 Single nu

ALIGNMENTS

RESULT 1
ID AA166582 standard; DNA; 20 BP.
XX
AC AA166582;
DT 11-DEC-2001 (first entry)
XX
DE Oculocutaneous albinism 1B causative gene related PCR primer #2.
XX
DE Hamster; oculocutaneous albinism 1B; tyrosinase; OCA1B;
KW pigment sedimentation; ocular function; PCR primer; ss.
XX
OS Unidentified.
XX
PN JP200112483-A.
XX
PD 24-APR-2001.
XX
PF 18-OCT-1999; 99JP-00295686.
XX
PR 18-OCT-1999; 99JP-00295686.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
WP1; 2001-372654/39.
XX
PT An ocular-cutaneous albinism 1B causative gene and its application.
XX
PS Example 5; Page 7; 17pp; Japanese.
CC The present invention relates to a transgenic animal, particularly a
CC hamster, which has a mutant version of the oculocutaneous albinism 1B
CC (OCA1B) causative gene. The protein encoded by this gene is a tyrosinase,
CC which can be detected in the animal. It can also be used in the
CC prevention, diagnosis and treatment of OCA1B, and to investigate
CC mechanisms in pigment sedimentation and ocular function. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 71.4%; Score 15; DB 4; Length 20;

*Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GACCTGCCAGGCTC 18
Db 20 GACCTGCCAGGCTC 6

RESULT 2

ADP68070/C
ID ADP68070 standard; DNA; 20 BP.

AC ADP68070;

DT 12-AUG-2004 (first entry)

DE Human jagged 1 target oligonucleotide #1.

XX Jagged 1; serrate gene; JAG 1; HJ1; AGS; AMD; AMS; diagnosis;
KW hyperproliferative disorder; developmental disorder; cytostatic; therapy;
KW human; ss.

XX Homo sapiens.

OS US2004102401-A1.

PN 27-MAY-2004.

PD 22-NOV-2002; 2002US-00304082.

PE 22-NOV-2002; 2002US-00304082.

PR 22-NOV-2002; 2002US-00304082.

PA (ISIS-) ISIS PHARM INC.

PI Dean NM, Bennett CF, Dobie KW;

DR WPI; 2004-399731/37.

XX New compound targeted to a nucleic acid molecule encoding jagged 1,
PT useful in diagnosing and treating hyperproliferative disorder.

XX Example 15; SEQ ID NO 48; 40pp; English.

XX The present invention is directed to antisense oligonucleotides targeted
CC to jagged 1 (also known as serrate gene, JAG1, HJ1, AGS, AMD and AMS) and
CC which modulate the expression of jagged 1. The invention is useful in
CC diagnosing and treating hyperproliferative and developmental disorders.
CC The invention acts as a cytostatic agent. The present sequence is human
CC jagged 1 target oligonucleotide. This sequence is used in the
CC exemplification of the invention.

XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 64.8%; Score 13.6; DB 12; Length 20;

Best Local Similarity 70.0%; Pred. No. 8.2e+03;

Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCTGCCAGGCTCATT 21
Db 20 AGGACCTGCCAGGCTCATT 1

RESULT 3

ADP68033
ID ADP68033 standard; DNA; 20 BP.

AC ADP68033;

DT 12-AUG-2004 (first entry)

DE Human jagged 1 antisense oligonucleotide ISIS #171243.

XX Jagged 1; serrate gene; JAG 1; HJ1; AGS; AMD; AMS; diagnosis;

KW hyperproliferative disorder; developmental disorder; cytostatic; therapy;
KW human; antisense; phosphorothioate backbone; ss.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone where all cytidines are

FT 5-methyl cytidines"

FT modified_base 1..5

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX US2004102401-A1.

XX 27-MAY-2004.

XX 22-NOV-2002; 2002US-00304082.

XX 22-NOV-2002; 2002US-00304082.

XX 22-NOV-2002; 2002US-00304082.

XX (ISIS-) ISIS PHARM INC.

XX Dean NM, Bennett CF, Dobie KW;

XX WPI; 2004-399731/37.

XX New compound targeted to a nucleic acid molecule encoding jagged 1,
PT useful in diagnosing and treating hyperproliferative disorder.

XX Example 15; SEQ ID NO 11; 40pp; English.

XX The present invention is directed to antisense oligonucleotides targeted
CC to jagged 1 (also known as serrate gene, JAG1, HJ1, AGS, AMD and AMS) and
CC which modulate the expression of jagged 1. The invention is useful in
CC diagnosing and treating hyperproliferative and developmental disorders.
CC The invention acts as a cytostatic agent. The present sequence is human
CC jagged 1 antisense oligonucleotide. This sequence is used in the
CC exemplification of the invention.

XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 64.8%; Score 13.6; DB 12; Length 20;

Best Local Similarity 70.0%; Pred. No. 8.2e+03;

Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCTGCCAGGCTCATT 21
Db 1 AGGACCTGCCAGGCTCATT 20

RESULT 4

ADH64423
ID ADH64423 standard; DNA; 20 BP.

AC ADH64423;

DT 25-MAR-2004 (first entry)

DE Human glucocorticoid receptor-specific antisense oligonucleotide #1257.

XX antisense oligonucleotide; glucocorticoid receptor; infection;
KW inflammation; tumour formation; diabetes; obesity;
KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX Homo sapiens.
 OS
 XX WO2003099215-A2.
 PN
 XX
 XX
 XX
 PD 04-DEC-2003.
 PF 20-MAY-2003; 2003WO-US016084.
 XX
 XX 20-MAY-2002; 2002US-0381857P.
 PR
 XX (PHAA) PHARMACIA CORP.
 PA
 XX Crosby SD, Nalseth AE;
 PI
 XX WPI; 2004-035034/03.
 DR
 XX
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
 CC
 XX Claim 4; SEQ ID NO 1257; 985bp; English.
 PS
 XX The invention comprises an antisense oligonucleotide that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 CC
 SQ Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 12; Length 20;
 Best Local Similarity 61.1%; Pred. No. 1.3e+04;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 4 GACCGCCAGGCGCCTT 21
 |||:||||:||||:
 Db 2 GTCCTCCACGCTCTTT 19

RESULT 5
 ID ADH64554 standard; DNA; 20 BP.
 XX
 AC ADH64554;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 XX Human glucocorticoid receptor-specific antisense oligonucleotide #1386.
 DE
 XX
 XX antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX
 OS Homo sapiens.
 XX
 XX WO2003099215-A2.
 PN
 XX
 XX
 PD 04-DEC-2003.
 PF 20-MAY-2003; 2003WO-US016084.
 XX
 XX 20-MAY-2002; 2002US-0381857P.
 PR
 XX (PHAA) PHARMACIA CORP.
 PA
 XX Crosby SD, Nalseth AE;
 PI
 XX

DR WPI; 2004-035034/03.
 XX
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
 CC
 XX Claim 4; SEQ ID NO 1386; 985bp; English.
 PS
 XX The invention comprises an antisense oligonucleotide that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 CC
 SQ Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 12; Length 20;
 Best Local Similarity 61.1%; Pred. No. 1.3e+04;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 4 GACCGCCAGGCGCCTT 21
 |||:||||:||||:
 Db 3 GTCCTCCACGCTCTTT 20

RESULT 6
 ID ADH63908 standard; DNA; 20 BP.
 XX
 AC ADH63908;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 XX Human glucocorticoid receptor-specific antisense oligonucleotide #742.
 DE
 XX
 XX antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX
 OS Homo sapiens.
 XX
 XX WO2003099215-A2.
 PN
 XX
 XX
 PD 04-DEC-2003.
 PF 20-MAY-2003; 2003WO-US016084.
 XX
 XX 20-MAY-2002; 2002US-0381857P.
 PR
 XX (PHAA) PHARMACIA CORP.
 PA
 XX Crosby SD, Nalseth AE;
 PI
 XX WPI; 2004-035034/03.
 DR
 XX
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.
 CC
 XX Claim 4; SEQ ID NO 742; 985bp; English.
 PS
 XX The invention comprises an antisense oligonucleotide that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 CC

CC the human glucocorticoid receptor gene. NOTE: The present sequence
CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
XX
SQ Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 62.9%; Score 13.2; DB 12; Length 20;
Best Local Similarity 61.1%; Pred. No. 1.3e+04;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 4 GACCGGCGAGGCGUCUTT 21
|||:||||:||||:
Db 1 GTCTTCACGCTGCTCTT 18

RESULT 7
ADL48810
ID ADL48810 standard; RNA, 17 BP.

AC ADL48810;

DT 20-MAY-2004 (first entry)

DE Human IKK-gamma substrate sequence #1320.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW resectosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
KW substrate; ds.

XX Unidentified.

XX WO200281628-A2.

PD 17-OCT-2002.

PF 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fornaugh K;

DR WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 2343; 317bp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC resectosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human IKK-
CC gamma substrate sequence.

XX
SQ Sequence 17 BP; 2 A; 5 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 UAGACCGGCGAGGCG 16
|||||
Db 2 UAGGCGCGCGCGAGGCG 17

RESULT 8
ADL48391
ID ADL48391 standard; RNA, 17 BP.

AC ADL48391;

DT 20-MAY-2004 (first entry)

DE Human IKK-gamma substrate sequence #901.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW resectosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
KW substrate; ds.

XX Unidentified.

XX WO200281628-A2.

PD 17-OCT-2002.

PF 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

PR 29-MAY-2001; 2001US-0294412P.

PR 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fornaugh K;

DR WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 1924; 317bp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC resectosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human IKK-
CC gamma substrate sequence.

XX Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 11; Length 17;

Best Local Similarity 87.5%; Pred. No. 2e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGGACCCGCGCAGUC 16

DB 1 UAGGACCCGCGCAGUC 16

RESULT 9

ADL14399 ADL14399 standard; DNA; 19 BP.

AC ADL14399;

DT 20-MAY-2004 (first entry)

DE PCR primer used to amplify the UGT Y486D isoform SeqID 8.

XX drug metabolic ability; UGT; UDP-glucuronosyl transferase;

KW gene analysis; liver function; Crigler-Najjar syndrome type I;

KW Crigler-Najjar syndrome type II; Gilbert syndrome;

KW Dublin-Johnson syndrome; Rotor syndrome; PCR; primer; ss.

OS Synthetic.

PN WO2004016814-A1.

XX 26-FEB-2004.

PF 13-FEB-2003; 2003WO-JP001475.

PR 12-AUG-2002; 2002JP-00235029.

PA (UTNI-) UNIV JAPAN SEC SHIGA MED.

PI Sato H, Fujiyama Y, Yamamoto K;

DR WPI; 2004-203813/19.

XX Estimation of drug metabolic activity by analyzing mutations in

PT glucuronosyltransferase gene, useful in studying drug metabolism, gene

PT analysis and clinical examination e.g. of diseases.

PS Disclosure; SEQ ID NO 8; 33pp; Japanese.

XX This invention relates to a novel method for examining the drug metabolic

CC ability of UGT (UDP-glucuronosyl transferase). Specifically, it refers

CC to the use of nucleic acid chips and/or arrays with an appropriate

CC oligonucleotide probe to detect mutations existing in exon 5 of the UGT

CC gene. The present invention describes the method as useful for studying

CC drug metabolism, gene analysis and for the clinical examination of

CC diseases that are associated with abnormal liver function including

CC Crigler-Najjar syndrome types I and II, Gilbert syndrome, Dublin-Johnson

CC syndrome and Rotor syndrome. This oligonucleotide sequence is a PCR

CC primer used to amplify a UGT DNA isoform, given in an exemplification of

CC the invention.

XX Sequence 19 BP; 2 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 12; Length 19;

Best Local Similarity 68.8%; Pred. No. 2e+04; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGACCTGCGCAGTCTC 18

DB 4 GGACCTGCGCAGTCTC 19

RESULT 10

AAF69353 AAF69353 standard; DNA; 20 BP.

XX AAF69353;

AC 18-APR-2001 (first entry)

DE Integrin-linked kinase 3'UTR targeted oligonucleotide #2.

KW Antisense; integrin-linked kinase; hIK; infection; tumour; inflammation;

KW ss.

OS Homo sapiens.

PN US6177273-B1.

PD 23-JAN-2001.

PF 26-OCT-1999; 99US-00428219.

PR 26-OCT-1999; 99US-00428219.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowse LM;

DR WPI; 2001-137069/14.

XX Novel antisense compounds capable of modulating expression of human

PT integrin-linked kinase, useful for diagnosis, prophylaxis and treatment

PT of diseases, e.g. tumors, associated with expression of the kinase.

PS Claim 3; Col 45; 40pp; English.

XX The present invention relates to an antisense compound 8 to 30 bases in

CC length targeted to the 5' untranslated (UTR) region, the coding region or

CC the 3' UTR region human integrin-linked kinase (hIK). The antisense

CC oligonucleotides are useful for inhibiting the expression of human hIK in

CC human cells or tissues, in vitro. The oligonucleotides can be utilized

CC for diagnostics, therapeutics for the treatment of diseases associated

CC with the expression of hIK, prophylaxis e.g. to prevent or delay

CC infection, inflammation or tumor formation and as research reagent

XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 4; Length 20;

Best Local Similarity 68.8%; Pred. No. 2e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGGACCTGCGCAGTCTC 17

DB 3 AGGACCTGCGCAGTCTC 18

RESULT 11

ADBE43705/c ADBE43705 standard; DNA; 20 BP.

XX ADBE43705;

XX 29-JAN-2004 (first entry)

DE Human KNSL1 sequencing primer, SEQ ID 310.

XX Neurodegenerative disease; uPA; SNGC; IDE; KNSL1; LIPA; TNFRSF6;

KW Alzheimer's disease; neuroprotective; nootropic; gene therapy;

KW Chromosome 10; PCR; primer; ss.

OS Homo sapiens.

PN WO2003054143-A2.


```
PR 09-NOV-2001; 2001US-0338363P.
PR 04-DEC-2001; 2001US-0337052P.
PR 28-MAR-2002; 2002US-0368919P.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Becker KD, Veliceljebl G, Elliott KJ, Wang X, Tanzi RE;
XX Berram L, Saunders AJ, Mullin KM, Sampson AJ;
XX WPI; 2004-060538/06.
XX
XX Determining a predisposition for or the occurrence of neurodegenerative
XX disease, particularly Alzheimer's disease, comprises determining the
XX presence of a polymorphism in the uPA, SNCG, IDE, KNSL1, LIPA or TNFRSF6
XX gene.
XX
XX Example 3; SEQ ID NO 310; 205bp; English.
XX
XX This invention relates to a novel method of determining a predisposition
XX for or the occurrence of neurodegenerative disease comprising detecting
XX in a target nucleic acid obtained from the subject the presence of an
XX allelic variant of polymorphic regions of human genes selected from
XX urokinase plasminogen activator (uPA), gamma-synuclein (SNCG), insulin
XX degrading enzyme (IDE), kinesin-like protein 1 (KNSL1), lysosomal acid
XX lipase (LIPA) and tumour necrosis factor receptor SF6 (TNFRSF6). The
XX method is useful in determining the presence or predisposition to a
XX neurodegenerative disease, particularly Alzheimer's disease. The present
XX sequence is that of a sequencing primer which was used for sequencing of
XX a region of the human KNSL1 gene in the exemplification of the invention.
XX
XX Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 61.0%; Score 12.8; DB 12; Length 20;
XX Best Local Similarity 68.8%; Pred. No. 2e+04;
XX Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 UAGGACGCGCCAGC 16
XX :|||:|||:|||
XX 16 TAGGTCCTGCCCATGTC 1
XX
XX RESULT 14
XX ADH64371
XX ADH64371 standard; DNA; 20 BP.
XX
XX ADH64371;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human glucocorticoid receptor-specific antisense oligonucleotide #1205.
XX
XX antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX phosphorochioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX Homo sapiens.
XX
XX WO2003099215-A2.
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016084.
XX
XX 20-MAY-2002; 2002US-0381857P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Crooby SD, Naleeth AE;
XX WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
```

```
PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 1205; 985bp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorochioate backbone.
XX
XX Sequence 20 BP; 3 A; 7 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 61.0%; Score 12.8; DB 12; Length 20;
XX Best Local Similarity 62.5%; Pred. No. 2e+04;
XX Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX 6 CCGGCGAGGCGCCTT 21
XX :|||:|||:|||
XX 1 CCTTCACTGCTCTTT 16
XX
XX RESULT 15
XX ADH63823
XX ADH63823 standard; DNA; 20 BP.
XX
XX ADH63823;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human glucocorticoid receptor-specific antisense oligonucleotide #657.
XX
XX antisense oligonucleotide; glucocorticoid receptor; infection;
XX inflammation; tumour formation; diabetes; obesity;
XX cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
XX phosphorochioate backbone; 2'-methoxyethyl; 2'-MOE.
XX
XX Homo sapiens.
XX
XX WO2003099215-A2.
XX
XX 04-DEC-2003.
XX
XX 20-MAY-2003; 2003WO-US016084.
XX
XX 20-MAY-2002; 2002US-0381857P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Crooby SD, Naleeth AE;
XX WPI; 2004-035034/03.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
XX cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
XX
XX Claim 4; SEQ ID NO 657; 985bp; English.
XX
XX The invention comprises an antisense oligonucleotides that are targeted
XX to nucleic acids encoding a mammalian glucocorticoid receptor. The
XX antisense oligonucleotides of the invention are useful for preventing or
XX delaying infection, inflammation or tumour formation. The antisense
XX oligonucleotides are also useful for treating diabetes, obesity,
XX cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
XX present DNA sequence represents an antisense oligonucleotide that targets
XX the human glucocorticoid receptor gene. NOTE: The present sequence
XX contains 2'-methoxyethyl (2'-MOE) wings and a phosphorochioate backbone.
```

SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 12; Length 20;

Best Local Similarity 62.5%; Pred. No. 2e+04; 2; Indels 0; Gaps 0;

Matches 10; Conservative 4; Mismatches 2;

QY 6 CCUGCCAGUGCUCUTT 21

DB 2 CCTCCACTGCTCTTT 17

Search completed: September 17, 2005, 10:22:12
Job time : 266 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 09:50:06 ; Search time 1907 Seconds
(without alignments)
419.166 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uagagccugccagcugcucut 21

Scoring table: IDENTITY_NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Database : Maximum Match 100%
Listing first 45 summaries

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_hic: *
4: gb_esc3: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_ges1: *
9: gb_ges2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.4	59.0	20	8	AZ496283 IM0332D09
2	11.4	54.3	19	8	AZ482658
3	10.2	48.6	20	8	AZ398062 IM0163M14
4	10	47.6	20	7	CF337542 JMT--08-A
5	9.8	46.7	19	8	AZ848554
6	9.8	46.7	19	8	AZ848554 2M0149A07
7	9.6	45.7	18	1	A1042533
8	9.6	45.7	18	1	A1042533 cyo6e03.x
9	9.4	44.8	11	5	BQ592717 E012124-0
10	9.4	44.8	19	8	AZ772446 IM0583O16
11	9.4	44.8	20	8	AZ625776
12	9.2	43.8	16	9	CL657853
13	9.2	43.8	20	8	AZ827759
14	9.2	43.8	20	8	AZ827759 2M0104E22
15	9.2	43.8	20	9	AJ591869
16	9.2	43.8	21	8	AZ611719
17	9.2	43.8	19	8	AZ611719 IM0540M24
18	9.2	43.8	21	8	AZ611719 IM0540M24
19	9.2	43.8	21	8	AZ611719 IM0540M24
20	9.2	43.8	21	8	AZ611719 IM0540M24
21	9.2	43.8	21	8	AZ611719 IM0540M24
22	9.2	43.8	21	8	AZ611719 IM0540M24
23	9.2	43.8	21	8	AZ611719 IM0540M24
24	9.2	43.8	21	8	AZ611719 IM0540M24

25	8.8	41.9	20	8	AZ833768	AZ833768 2M0116002
26	8.8	41.9	21	1	AJ747329	AJ747329 AJ747329
27	8.8	41.9	21	4	BM398777	BM398777 5009-0-5-
28	8.8	41.9	21	8	AZ342282	AZ342282 IM0075H14
29	8.8	41.9	21	8	AZ581771	AZ581771 IM0370P10
30	8.6	41.0	17	7	CF310268	CF310268 ABF--04-N
31	8.6	41.0	18	8	AQ026356	AQ026356 1(3)rg554
32	8.6	41.0	19	7	CF307006	CF307006 HDAl--06-
33	8.6	41.0	19	7	CF307304	CF307304 HDAl--06-
34	8.6	41.0	19	7	CF307439	CF307439 HDAl--06-
35	8.6	41.0	19	8	AZ839439	AZ839439 2M0135L06
36	8.6	41.0	20	1	AJ652453	AJ652453 AJ652453
37	8.6	41.0	20	7	CF307027	CF307027 HDAl--05-
38	8.6	41.0	20	7	CF307258	CF307258 HDAl--06-
39	8.6	41.0	20	8	AZ946089	AZ946089 2M0207A13
40	8.6	41.0	20	8	AZ02281	AZ02281 Pan ctrog1
41	8.6	41.0	21	7	CF307437	CF307437 HDAl--06-
42	8.6	41.0	21	8	AZ862876	AZ862876 2M0170B18
43	8.6	41.0	21	9	AG196285	AG196285 Pan ctrog1
44	8.6	41.0	21	9	AG202462	AG202462 Pan ctrog1
45	8.6	41.0	21	9	AJ587178	AJ587178 Arabidops

ALIGNMENTS

RESULT 1
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

AZ496283 20 bp DNA linear GSS 05-OCT-2000
1M0332D09R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0332D09 R, genomic survey sequence.
AZ496283
AZ496283.1 GI:10672347
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0332 row: D column: 09
Seq primer: CACACGAGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0332D09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.0%; Score 12.4; DB 8; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.9e+05;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 CUGCCAGUCUCUT 20
| | | | | : | | | | |
Db 1 CAGCCAGTCTCTT 14

RESULT 2

AZ482658/c 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M030716R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M030716 R, genomic survey sequence.

ACCESSION AZ482658
VERSION AZ482658.1 GI:10645919
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0307 row: L column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 19.
Location/Qualifiers

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M030716"

FEATURES

source

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.3%; Score 11.4; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 8.8e+05;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACCUGCCAGUCU 17
| | | | | : | | | | |
Db 13 ACTGCCAGAGCT 1

RESULT 3

A2398062/c 20 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0163M14F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0163M14 F, genomic survey sequence.

ACCESSION A2398062
VERSION A2398062.1 GI:10513134
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: M column: 14
Seq primer: CGTTGAAGACAGCGCCAGT
Class: plasmid ends

High quality sequence stop: 20.
Location/Qualifiers

1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0163M14"

FEATURES

source

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 48.6%; Score 10.2; DB 8; Length 20;
Best Local Similarity 60.0%; Pred. No. 3.4e+06;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 3 GGACCGCAGGUCU 17
|||:|||||:
Db 19 GGCCCTGCTGCT 5

RESULT 4
LOCUS CF337542 20 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--08-A10.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--08-A10, mRNA sequence.
CF337542 GI:33823470
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

TITLE JOURNAL
COMMENT

FEATURES

source
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/lab_host="E.coli DH10B"
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/note="Vector: PCR4-TOPO, Site 1: EcoRI, Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis jasmonate Carboxyl methyltransferase overexpression line."

ORIGIN

Query Match 47.6%; Score 10; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 3 GGACCGCAGGUCUCU 20
|||:|||||:
Db 2 GGTCATGACAGTGT 19

RESULT 5
LOCUS AZ848554 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0149A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0149A07 R, genomic survey sequence.
AZ848554
AZ848554.1 GI:13031758
GSS.

ACCESSION
VERSION
KEYWORDS
MUS musculus (house mouse)

REFERENCE

AZ848554
1 (bases 1 to 19)
Dunn,D., Moyagi,A., Barber,M., Beacom,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0149 row: A column: 07
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

JOURNAL

COMMENT

FEATURES

source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0149A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 46.7%; Score 9.8; DB 8; Length 19;
Best Local Similarity 53.8%; Pred. No. 5.2e+06;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 CUGCCAGUGUCUCU 19
 ||:|||||:|:
 Db 3 CTGCTAGTCTCTGT 15

RESULT 6
 A2868070 19 bp DNA linear GSS 21-FEB-2001
 LOCUS A2868070/c
 DEFINITION 2M0179107F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0179107 F, genomic survey sequence.

ACCESSION A2868070
 VERSION A2868070.1 GI:13071017
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 19)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0179 row: I column: 07
 Seq primer: CGTGTAAACGACGCCGCACT
 Class: Plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:10090"
 /clone="UGCGM0179107"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 46.7%; Score 9.8; DB 8; Length 19;
 Best Local Similarity 53.8%; Pred. No. 5.2e+06;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 CUGCCAGUGUCUCU 19
 ||:|||||:|:
 Db 15 CTGCTAGTCTCTGT 3

RESULT 7
 A1042533/c 18 bp mRNA linear EST 30-JUN-1998
 LOCUS A1042533
 DEFINITION cy06e03.x1 Soares senescent fibroblasts NHHSF Homo sapiens cDNA
 clone IMAGE:1665052.3 similar to TR:Q15662 Q15662
 TRANSFORMATION-RELATED PROTEIN /, mRNA sequence.

ACCESSION A1042533
 VERSION A1042533.1 GI:3281727
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 18)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

TITLE Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source 1..18
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1665052"
 /clease_type="senescent fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares senescent fibroblasts_NHHSF"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker V-type: phagemid; Site 1: Not I; Site 2: Eco
 RI; 1st strand cDNA was primed with a Not I - oligo (dT)
 primer [5',
 TGTACCAATCTGAAGGAGGCGCCGATTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 45.7%; Score 9.6; DB 1; Length 18;
 Best Local Similarity 56.2%; Pred. No. 6.5e+06;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 CUGCCAGUGUCUCU 21
 ||:|||||:|:
 Db 17 CTTTCAGTCTCTGT 2

RESULT 8
 A2656028 21 bp DNA linear GSS 14-DEC-2000
 LOCUS A2656028
 DEFINITION IM0531017F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0531017 F, genomic survey sequence.

ACCESSION A2656028
 VERSION A2656028.1 GI:11793174
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 21)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0179 row: I column: 07
 Seq primer: CGTGTAAACGACGCCGCACT
 Class: Plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0531 row: 0 column: 17
Seq primer: CGTGTAAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0531017"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: pMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gt|473214|gb|AF19072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 45.7%; Score 9.6; DB 8; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.6e+06;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 6 CCUGCCAGUCUCUUTT 21
||:||||:|
Db 5 CCTACAGTCTTAT 20

RESULT 9
BQ592717/c 11 bp mRNA linear EST 06-DEC-2002
LOCUS E012124-024-028-J16-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
DEFINITION cDNA clone 024-028-J16 5-PRIME, mRNA sequence.
ACCESSION BQ592717
VERSION BQ592717.1 GI:26122300
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 11)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radeflof,U.
TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 28 row: J column: 16
Seq primer: SP6, CATACGATTGATGACACTATAG.
Location/Qualifiers
1. .11
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:194137"
/db_xref="taxon:161934"
/clone="024-028-J16"
/issue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzehnleberer Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZP/GABI-Primary database: http://gabi.rzp.de"

ORIGIN
Query Match 44.8%; Score 9.4; DB 5; Length 11;
Best Local Similarity 72.7%; Pred. No. 7.6e+06;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 5 ACCUGCCAGUC 15
||:||||:|
Db 11 ACCTACGAGT 1

RESULT 10
A2772446 19 bp DNA linear GSS 16-FEB-2001
LOCUS I00583016F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0583016 F, genomic survey sequence.
ACCESSION A2772446
VERSION A2772446.1 GI:12895762
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: 0 column: 16
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0583016"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 44.8%; Score 9.4; DB 8; Length 19;
Best Local Similarity 72.7%; Pred. No. 8.2e+06;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 5 ACCUGCCAGUG 15
|||:|||||
6 ACCTGACAGTG 16

RESULT 11
A2625776 20 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0465C08R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0465C08 R, genomic survey sequence.
ACCESSION A2625776
VERSION A2625776.1 GI:11747966
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Mennen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0465 row: C column: 08
Seq primer: CACACAGAAACACTATGAC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0465C08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 44.8%; Score 9.4; DB 8; Length 20;
Best Local Similarity 47.4%; Pred. No. 8.2e+06;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 UAGGACCGCCAGUGUCU 19
:|||||:|||||:
19 TAGAATCTTGAAAGCGCCT 1

RESULT 12
CL657853 16 bp DNA linear GSS 09-JUN-2004
LOCUS PR1012C_H07 - PR1012C.B21 (16) Mixed strage. fomicd library of P. pacificus var. California Pristionchus pacificus genomic, genomic
DEFINITION survey sequence.
ACCESSION CL657853
VERSION CL657853.1 GI:50139888
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
1 (bases 1 to 16)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Appad: an Acced database for the nematode satellite organism
TITLE Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL Contact: Sommer RJ
COMMENT Evolutionary Biology

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES

source

Location/Qualifiers
1..16
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pB1fos-5 Fosmid vector"

ORIGIN

Query Match 43.8%; Score 9.2; DB 9; Length 16;
Best Local Similarity 50.0%; Pred. No. 1e+07; 3; Indels 0; Gaps 0;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 8 UGCCAGUCGUCUTT 21
:||||:|:|:
Db 3 TACCAGTACTCTCT 16

RESULT 13
A2827759/c 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0104222F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
LOCUS clone UUGC2M0104E22 F, genomic survey sequence.
ACCESSION A2827759
VERSION A2827759.1 GI:12997667
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: E column: 22
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC2M0104E22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/anates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-replicated with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 8; Length 20;
Best Local Similarity 57.1%; Pred. No. 1e+07; 3; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 8 UGCCAGUCGUCUTT 21
:||||:|:|:
Db 20 TCCAGTGCAGT 7

RESULT 14
AJ591869/c 20 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
LOCUS 594C10, genomic survey sequence.
ACCESSION AJ591869
VERSION AJ591869.1 GI:37941493
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepoint, L., Caboche, M. and Leclercq, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
Balzerque, S.
2 (bases 1 to 20)
12446565
Balzerque, S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (6) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES

source

Location/Qualifiers
1..20
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassiljewskij4"
/db_xref="taxon:3702"

/clone="594C10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1..20="T-DNA flanking sequence
/note="T-DNA flanking sequence
left border"

ORIGIN

Query Match 43.8%; Score 9.2; DB 9; Length 20;
Best Local Similarity 71.4%; Pred. No. 1e+07; Mismatches 3; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 5 ACCUGCCAGUGC 18
|||:|
17 ACTAGCCAGTGCAC 4

Db 17 ACTAGCCAGTGCAC 4

RESULT 15
A2661719 21 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0540M24F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0540M24 F, genomic survey sequence.

ACCESSION A2661719
VERSION A2661719.1 GI:11798865
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

JOURNAL

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std. Error: 0.00
Plate: 0540 row: M column: 24

Seq primer: CATTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGIM0540M24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 8; Length 21;
Best Local Similarity 64.3%; Pred. No. 1e+07; Mismatches 3; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 2 AGGACUGCCAGUG 15
|||:|
5 AGGACGTGTAGTC 18

Db 5 AGGACGTGTAGTC 18

Search completed: September 17, 2005, 11:19:51
Job time : 1914 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 07:53:35; Search time 94 Seconds
(without alignments)
365.551 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 uagaccugccagucucucut 21

Scoring table: IDENTITY_NUC

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 457068

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.8	61.0	20	3	US-09-428-219-82
2	12.4	59.0	17	3	US-08-998-099-62
3	12.4	59.0	20	4	US-09-198-452A-6154
4	12.2	58.1	20	4	US-09-861-158-78
5	12	57.1	21	1	US-07-937-609-5
6	12	57.1	21	3	US-08-029-170-5
7	12	57.1	21	4	US-09-443-745-5
8	12	57.1	21	4	US-09-657-472-877
9	11.8	56.2	20	3	US-09-702-327-53
10	11.8	56.2	20	3	US-09-517-467B-256
11	11.8	56.2	20	4	US-09-657-346A-69
12	11.8	56.2	20	4	US-09-900-920-12
13	11.8	56.2	21	4	US-09-657-472-1359
14	11.6	55.2	20	2	US-08-117-952-361
15	11.6	55.2	20	3	US-09-313-932-485
16	11.6	55.2	20	3	US-09-517-467B-337
17	11.6	55.2	20	4	US-09-198-452A-2895
18	11.4	54.3	17	1	US-08-152-313-113
19	11.4	54.3	17	1	US-08-579-223-113
20	11.4	54.3	17	4	US-09-474-433B-479
21	11.4	54.3	17	4	US-09-474-433B-859
22	11.4	54.3	17	4	US-09-476-387-478
23	11.4	54.3	17	4	US-09-476-387-858
24	11.4	54.3	17	5	PCT-US94-12947A-113
25	11.4	54.3	18	2	US-08-257-963B-35
26	11.4	54.3	18	3	US-08-367-841A-35
27	11.4	54.3	18	5	PCT-US95-07201-35

c	28	11.4	54.3	20	3	US-09-428-583-44	Sequence 44, Appl
c	29	11.4	54.3	20	4	US-09-844-634-57	Sequence 57, Appl
c	30	11.4	54.3	20	4	US-09-657-346A-40	Sequence 40, Appl
c	31	11.4	54.3	20	4	US-09-608-958-5	Sequence 5, Appl
c	32	11.4	54.3	20	4	US-09-422-978-5960	Sequence 5960, Ap
c	33	11.4	54.3	21	1	US-08-240-547-42	Sequence 42, Appl
c	34	11.2	53.3	17	2	US-08-292-620A-1886	Sequence 1886, Ap
c	35	11.2	53.3	17	2	US-08-292-620A-1977	Sequence 1977, Ap
c	36	11.2	53.3	17	3	US-09-071-845-1886	Sequence 1886, Ap
c	37	11.2	53.3	17	3	US-09-071-845-1977	Sequence 1977, Ap
c	38	11.2	53.3	19	3	US-09-522-800-11	Sequence 11, Appl
c	39	11.2	53.3	20	4	US-09-198-452A-6127	Sequence 6127, Ap
c	40	11.2	53.3	21	4	US-09-366-257-2	Sequence 2, Appl
c	41	11.2	53.3	21	4	US-09-422-978-11690	Sequence 11690, A
c	42	11.2	53.3	21	4	US-09-889-732-2	Sequence 2, Appl
c	43	11.2	53.3	21	4	US-08-278-774-29	Sequence 29, Appl
c	44	11	52.4	19	3	US-09-407-818-11	Sequence 11, Appl
c	45	11	52.4	19	4	US-09-696-791-1998	Sequence 1998, Ap

ALIGNMENTS

```
RESULT 1
US-09-428-219-82
Sequence 82, Application US/09428219
Patent No. 6177273
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
FILE REFERENCE: RUS-0101
CURRENT APPLICATION NUMBER: US/09/428,219
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 82
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-09-428-219-82

Query Match      61.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 68.8%; Pred. No. 5.5e+03;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 AGGACCGUCGAGUCU 17
      |||||:||||:
Db      3 AGGACCTTCAGTCT 18

RESULT 2
US-08-998-099-62/c
Sequence 62, Application US/08998099A
Patent No. 6103890
GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: MCSWIGEN, JAMES A.
APPLICANT: STINCHCOMB, DAN T.
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
FILE REFERENCE: 231/175
CURRENT APPLICATION NUMBER: US/08/998,099A
CURRENT FILING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 08/373,124
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 08/245,466
EARLIER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FASTSEQ for Windows Version 3.0
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SEQ ID NO 62
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-08-998-099-62

Query Match
Best Local Similarity 59.0%; Score 12.4; DB 3; Length 17;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCUGCCAGUCUCU 19
DB 15 CCTGCCAATGCTCT 2

RESULT 3
US-09-198-452A-6154/C
Sequence 6154, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffeis, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 6154
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6154

Query Match
Best Local Similarity 59.0%; Score 12.4; DB 4; Length 20;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 UGCGAGUCUCU 21
DB 15 TGCCTGCTCTTT 2

RESULT 4
US-09-861-159-78/C
Sequence 78, Application US/09861159
Patent No. 6485974
GENERAL INFORMATION:
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN2 EXPRESSION
FILE REFERENCE: RTS-0243
CURRENT APPLICATION NUMBER: US/09/861,159
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 78
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-861-159-78

Query Match
Best Local Similarity 58.1%; Score 12.2; DB 4; Length 20;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 UAGACUCGCGAGUCU 17
DB 20 TAGTACTGACAGTCT 4

RESULT 5

US-07-937-609-5/C
Sequence 5, Application US/07937609
Patent No. 5319073
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NTHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-937-609-5

Query Match
Best Local Similarity 57.1%; Score 12; DB 1; Length 21;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGCCAGUCUC 18
DB 16 CTGCCAGTCTC 5

RESULT 6
US-08-029-170-5/C
Sequence 5, Application US/08029170
Patent No. 6169173
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA

ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA

```
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/029,170
FILING DATE: 19930310
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-08-029-170-5

Query Match      57.1%; Score 12; DB 3; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 CUGCCAGUGCUC 18
DB      16 CTGCCAGTGCCTC 5

RESULT 7
US-09-443-745-5/C
Sequence 5, Application US/09443745
Patent No. 6706493
GENERAL INFORMATION:
APPLICANT: MANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECTOSTOLININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443,745
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-443-745-5
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Query Match      57.1%; Score 12; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 CUGCCAGUGCUC 18
DB      16 CTGCCAGTGCCTC 5
```

```
RESULT 8
US-09-657-472-877
Sequence 877, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolk, Stacey
APPLICANT: Daley, George O.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT APPLICATION NUMBER: US/09/657,472
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 877
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-657-472-877
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```
Query Match      57.1%; Score 12; DB 4; Length 21;
Best Local Similarity 64.3%; Pred. No. 1.4e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY      6 CUGCCAGUGCUCU 19
DB      11 CTGCCAGTGCCTC 5
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Db' 1 CCTGCCAGTGYCCT 14

RESULT 9
US-09-702-327-53
; Sequence 53, Application US/09702327
; Patent No. 6426220
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION
; FILE REFERENCE: RTS-0097
; CURRENT APPLICATION NUMBER: US/09/702,327
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-327-53

Query Match 56.2%; Score 11.8; DB 3; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCCGCCAGGCGCUC 18
Db 5 GACCTGCCAGAGGCTC 19

RESULT 10
US-09-517-467B-256/C
; Sequence 256, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
; FILE REFERENCE: RTS-0150
; CURRENT APPLICATION NUMBER: US/09/517,467B
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 256
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-467B-256

Query Match 56.2%; Score 11.8; DB 3; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 URGACCTGCCAGUG 15
Db 19 TAGGACCGCAAGTG 5

RESULT 11
US-09-657-346A-69
; Sequence 69, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
; FILE REFERENCE: RTS-0135

; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-346A-69

Query Match 56.2%; Score 11.8; DB 4; Length 20;
Best Local Similarity 73.3%; Pred. No. 1.7e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCCGCCAGGCGCUC 18
Db 4 GACATGCCAGGGCTC 18

RESULT 12
US-09-900-920-12/C
; Sequence 12, Application US/09900920
; Patent No. 6696562
; GENERAL INFORMATION:
; APPLICANT: Schultz-Cherry, Stacey
; APPLICANT: Kelley, Laura
; APPLICANT: Koci, Matthew
; TITLE OF INVENTION: No. 6696562e1 Avian Astrovirus
; FILE REFERENCE: turkeyastrovirus
; CURRENT APPLICATION NUMBER: US/09/900,920
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,312
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Turkey Astrovirus
US-09-900-920-12

Query Match 56.2%; Score 11.8; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 CUGCCAGGCGCUTT 21
Db 17 CTGCCAGTGGTCATT 3

RESULT 13
US-09-657-472-1359/C
; Sequence 1359, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George O.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2551
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1359
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-657-472-1359

Query Match 56.2%; Score 11.8; DB 4; Length 21;
 Best Local Similarity 64.7%; Pred. No. 1.7e+04;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AGGACCGCCAGUCGUC 18
 Db 18 AGGCTCTCCAGAGCTC 2

RESULT 14
 US-08-117-952-361/c
 Sequence 361, Application US/08117952
 Patent No. 5851760
 GENERAL INFORMATION:
 APPLICANT: Evans, Glen A.
 APPLICANT: Smith, Michael W.
 TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
 TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
 NUMBER OF SEQUENCES: 797
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 STREET: 444 South Flower Street, Suite 2000
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/117,952
 FILING DATE: 07-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/078,471
 FILING DATE: 15-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Reiter, Stephen E.
 REGISTRATION NUMBER: 31,192
 REFERENCE/DOCKET NUMBER: P41 9423
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-546-4737
 TELEFAX: 619-546-9392
 INFORMATION FOR SEQ ID NO: 361:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Oligonucleotide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-117-952-361

Query Match 55.2%; Score 11.6; DB 2; Length 20;
 Best Local Similarity 55.6%; Pred. No. 2.1e+04;
 Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GACCTGCGAGUCGUCUTT 21
 Db 18 GGCTGTGCGAGTGTATTT 1

RESULT 15
 US-09-313-932-485/c
 Sequence 485, Application US/09313932A
 Patent No. 6228642
 GENERAL INFORMATION:
 APPLICANT: Baker, Brenda
 APPLICANT: Bennett, C. Frank
 APPLICANT: Butler, Madeline M.
 APPLICANT: Shanahan, William R.
 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
 TITLE OF INVENTION: EXPRESSION
 FILE REFERENCE: ISPH-0356
 CURRENT APPLICATION NUMBER: US/09/313,932A
 CURRENT FILING DATE: 1999-05-18
 NUMBER OF SEQ ID NOS: 501
 SEQ ID NO 485
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-313-932-485

Query Match 55.2%; Score 11.6; DB 3; Length 20;
 Best Local Similarity 61.1%; Pred. No. 2.1e+04;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAGGACCTGCGAGUCGUC 18
 Db 18 TAGGAGCTGCGCTTGAGCTC 1

Search completed: September 17, 2005, 09:08:20
 Job time : 96 secs

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GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: September 17, 2005, 08:31:40 : Search time 390 Seconds
(without alignments)
358.754 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21
Sequence: 1 usagaccgcagcagucucut 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7389322 seqs, 331285599 residues

Total number of hits satisfying chosen parameters: 2069766

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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26:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-10-738-413-1	Sequence 1, Appl
2	18	85.7	20	US-10-424-041-41	Sequence 41, Appl
3	18	85.7	20	US-10-424-041-132	Sequence 132, Appl
4	17	81.0	20	US-10-424-041-56	Sequence 56, Appl
5	17	81.0	20	US-10-424-041-144	Sequence 144, Appl
6	13.6	64.8	20	US-10-304-082-11	Sequence 11, Appl
7	13.6	64.8	20	US-10-304-082-48	Sequence 48, Appl

c	8	13.6	64.8	21	US-10-847-918-2129	Sequence 2129, Ap
c	9	13.4	63.9	18	US-10-924-375-91	Sequence 91, Appl
c	10	13.2	62.9	20	US-11-039-629-89	Sequence 89, Appl
c	11	12.8	61.0	17	US-10-156-306-5959	Sequence 5959, Ap
c	12	12.8	61.0	17	US-10-156-306-7065	Sequence 7065, Ap
c	13	12.8	61.0	20	US-10-282-174-310	Sequence 310, Appl
c	14	12.8	61.0	20	US-10-188-883-82	Sequence 82, Appl
c	15	12.8	61.0	20	US-10-671-395-720	Sequence 720, Appl
c	16	12.8	61.0	20	US-10-671-395-995	Sequence 995, Appl
c	17	12.8	61.0	20	US-10-671-395-1209	Sequence 1209, Appl
c	18	12.8	61.0	20	US-10-671-395-1392	Sequence 1392, Appl
c	19	12.8	61.0	20	US-10-671-395-1473	Sequence 1473, Appl
c	20	12.8	61.0	20	US-10-600-009-310	Sequence 310, Appl
c	21	12.8	61.0	20	US-10-829-674-396	Sequence 396, Appl
c	22	12.8	61.0	20	US-10-830-477-396	Sequence 396, Appl
c	23	12.6	60.0	21	US-10-386-243-5	Sequence 5, Appl1
c	24	12.4	59.0	20	US-10-005-956-1172	Sequence 1172, Ap
c	25	12.4	59.0	20	US-10-289-762-6154	Sequence 6154, Ap
c	26	12.4	59.0	20	US-10-300-611-39	Sequence 39, Appl
c	27	12.4	59.0	20	US-10-671-395-957	Sequence 957, Appl
c	28	12.4	59.0	20	US-10-671-395-1552	Sequence 1552, Ap
c	29	12.2	58.1	19	US-10-665-951-1599	Sequence 1599, Ap
c	30	12.2	58.1	19	US-10-665-951-1846	Sequence 1846, Ap
c	31	12.2	58.1	19	US-10-758-155-1599	Sequence 1599, Ap
c	32	12.2	58.1	19	US-10-758-155-1846	Sequence 1846, Ap
c	33	12.2	58.1	19	US-10-831-620-1599	Sequence 1599, Ap
c	34	12.2	58.1	19	US-10-831-620-1846	Sequence 1846, Ap
c	35	12.2	58.1	19	US-10-844-076-1599	Sequence 1599, Ap
c	36	12.2	58.1	20	US-10-844-076-1846	Sequence 1846, Ap
c	37	12.2	58.1	20	US-10-475-146-78	Sequence 78, Appl
c	38	12.2	58.1	20	US-10-257-158A-6705	Sequence 6705, Ap
c	39	12.2	58.1	21	US-10-751-736-36179	Sequence 36179, A
c	40	12	57.1	17	US-09-818-875-1910	Sequence 1910, Ap
c	41	12	57.1	17	US-09-818-875-1911	Sequence 1911, Ap
c	42	12	57.1	17	US-09-818-875-1914	Sequence 1914, Ap
c	43	12	57.1	17	US-09-818-875-1915	Sequence 1915, Ap
c	44	12	57.1	17	US-10-209-787-1910	Sequence 1910, Ap
c	45	12	57.1	17	US-10-209-787-1911	Sequence 1911, Ap

ALIGNMENTS

RESULT 1
US-10-738-413-1
; Sequence 1, Application US/10738413
; Publication No. US20050137151A1
; GENERAL INFORMATION:
; APPLICANT: BINETTI, RALPH R.
; TITLE OF INVENTION: SI-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
; FILE REFERENCE: SC660-US
; CURRENT FILING DATE: 2003-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-738-413-1
Query Match 100.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGACCUGCCAGUCUUTT 21
|||
Db 1 UAGACCUGCCAGUCUUTT 21

RESULT 2
US-10-424-041-41/c
; Sequence 41, Application US/10424041
; Publication No. US20040215006A1

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GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Frelier
APPLICANT: Kenneth W. Doolie
TITLE OF INVENTION: MODULATION OF TYROSINASE
FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 41
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotides
US-10-424-041-41

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RESULT 3
US-10-424-041-132
; Sequence 132, Application US/10424041
; Publication No. US20040215006A1

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? GENERAL INFORMATION:
? APPLICANT: C. Frank Bennett
? APPLICANT: Thomas Condon
? APPLICANT: Susan M. Freiler
? APPLICANT: Kenneth W. Doble
? TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
? FILE REFERENCE: BIOL0005US
? CURRENT APPLICATION NUMBER: US/10/424,041
? CURRENT FILING DATE: 2003-04-25
? NUMBER OF SEQ ID NOS: 184
? SEQ ID NO 132
? LENGTH: 20
? TYPE: DNA
? ORGANISM: H. sapiens
? FEATURE:
? US-10-424-041-132

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RESULT 4
US-10-424-041-56/c
; Sequence 56, Application US/10424041-56/c
; Publication No. US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon

```

; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL000505
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-424-041-56

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Query	Match	Similarity	81.0%	Score 17	DB 20	Length 20
	Best Local	Similarity	76.5%	Pred. No. 1.1e+02		
Matches	13	Conservative	4	Mismatches	0	Indels 0
						Gaps 0
QY	1	UAGGACCTGCGCAGUGCU	17			
Db	17	TAGGACCTGCGCAGTCT	1			

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RESULT 5
US-10-424-041-144
; Sequence 144, Application US/10424041
; Publication No US20040215006A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIO000505
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 144
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
US-10-424-041-144

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Query Match	81.0%	Score 17;	DB 20;	Length 20;
Best Local Similarity	100.0%	Pred. No.	1.1e+02;	
Matches 17; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

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RESULT 6
US-10-304-082-11
; Sequence 11, Application US/10304082
; Publication No. US20040102401A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: PHS-0037
; CURRENT APPLICATION NUMBER: US/10/304,082
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

```

US-10-304-082-11

Query Match 64.8%; Score 13.6; DB 19; Length 20;
 Best Local Similarity 70.0%; Pred. No. 5.9e+03;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCCGACGAGGCTT 21
 Db 1 AGGACCTGCCAGGCTCAT 20

RESULT 7

US-10-304-082-48/c
 ; Sequence 48, Application US/10304082
 ; Publication No. US20040102401a1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Kenneth M. Doble
 ; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
 ; FILE REFERENCE: PTS-0037
 ; CURRENT APPLICATION NUMBER: US/10/304,082
 ; CURRENT FILING DATE: 2002-11-22
 ; NUMBER OF SEQ ID NOS: 78
 ; SEQ ID NO 48
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; US-10-304-082-48

Query Match 64.8%; Score 13.6; DB 19; Length 20;
 Best Local Similarity 70.0%; Pred. No. 5.9e+03;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCCGACGAGGCTT 21
 Db 20 AGGACCTGCCAGGCTCAT 1

RESULT 8

US-10-847-918-2129
 ; Sequence 2129, Application US/10847918
 ; Publication No. US20050119210a1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Be. Xiaobing
 ; APPLICANT: Liu, Wei
 ; APPLICANT: Slonim, Donna
 ; APPLICANT: Howes, Steve
 ; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
 ; FILE REFERENCE: 031896-026000 (AM101264)
 ; CURRENT APPLICATION NUMBER: US/10/847,918
 ; CURRENT FILING DATE: 2004-05-19
 ; PRIOR APPLICATION NUMBER: US 60/471,729
 ; PRIOR FILING DATE: 2003-05-20
 ; NUMBER OF SEQ ID NOS: 14937
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2129
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: RNAI-sense strand
 ; US-10-847-918-2129

Query Match 64.8%; Score 13.6; DB 21; Length 21;
 Best Local Similarity 75.0%; Pred. No. 6e+03; 4; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAGAGCCGACGAGGCTT 20
 Db 2 UCGAGCGCGAAGGCTT 21

RESULT 9

US-10-924-375-91/c
 ; Sequence 91, Application US/10924375
 ; Publication No. US20050130190a1
 ; GENERAL INFORMATION:
 ; APPLICANT: Antzelevitch, Charles
 ; APPLICANT: Brugada, Ramon
 ; APPLICANT: Hong, Kui
 ; TITLE OF INVENTION: Mutations in Ion Channel Proteins Associated with Sudden Cardiac
 ; FILE REFERENCE: 1396-2
 ; CURRENT APPLICATION NUMBER: US/10/924,375
 ; PRIOR APPLICATION NUMBER: 60/497,256
 ; PRIOR FILING DATE: 1998-08-22
 ; NUMBER OF SEQ ID NOS: 134
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 91
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: primer
 ; US-10-924-375-91

Query Match 63.8%; Score 13.4; DB 22; Length 18;
 Best Local Similarity 66.7%; Pred. No. 7.5e+03;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACCGCGACGAGGCTT 19
 Db 16 ACTGCGAGTCTGT 2

RESULT 10

US-11-039-629-89
 ; Sequence 89, Application US/11039629
 ; Publication No. US20050164271a1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bhanot, Sanjay
 ; APPLICANT: Doble, Kenneth W.
 ; APPLICANT: Freier, Susan M.
 ; APPLICANT: Dean, Nicholas M.
 ; APPLICANT: Bennett, C. Frank
 ; TITLE OF INVENTION: MODULATION OF GLUCOCORTICOID RECEPTOR
 ; FILE REFERENCE: RTS-0532US
 ; CURRENT APPLICATION NUMBER: US/11/039,629
 ; CURRENT FILING DATE: 2005-01-20
 ; PRIOR APPLICATION NUMBER: 60/538,173
 ; PRIOR FILING DATE: 2004-01-20
 ; PRIOR APPLICATION NUMBER: 60/550,191
 ; PRIOR FILING DATE: 2004-03-03
 ; NUMBER OF SEQ ID NOS: 310
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 89
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Compound
 ; US-11-039-629-89

Query Match 62.9%; Score 13.2; DB 24; Length 20;
 Best Local Similarity 61.1%; Pred. No. 9.5e+03;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GACCGCGACGAGGCTT 21
 Db 3 GTCCTCCAGTCTCTT 20

RESULT 11

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US-10-156-306-5959
; Sequence 5959, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSw19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MEBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5959

Query Match
Best Local Similarity 61.0%; Score 12.8; DB 15; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 UAGACCTGCGCCAGUGC 16
Db
1 UAGGCGCGCCAGUGC 16

RESULT 12
US-10-156-306-7065
; Sequence 7065, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSw19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MEBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7065
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7065

Query Match
Best Local Similarity 61.0%; Score 12.8; DB 15; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 UAGACCTGCGCCAGUGC 16
Db
2 UAGGCGCGCCAGUGC 17

RESULT 13
US-10-282-174-310/c
; Sequence 310, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelcibi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertiam, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
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; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-310

Query Match
Best Local Similarity 61.0%; Score 12.8; DB 17; Length 20;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY
1 UAGACCTGCGCCAGUGC 16
Db
16 TAGGTCTGCGCATTC 1

RESULT 14
US-10-188-883-82
; Sequence 82, Application US/10188883
; Publication No. US2004000605A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: USE OF INTEGRIN-LINKED KINASE INHIBITORS FOR TREATING INSULIN RESI
; FILE REFERENCE: ISPH-0687
; CURRENT APPLICATION NUMBER: US/10/188,883
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide.
US-10-188-883-82

Query Match
Best Local Similarity 61.0%; Score 12.8; DB 17; Length 20;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY
2 AGACCTGCGCCAGUGC 17
Db
3 AGACCTTCCAGTCT 18

RESULT 15
US-10-671-395-720/c
; Sequence 720, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
```

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; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 720
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-720

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Query Match      61.0%; Score 12.8; DB 19; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      6 CCUGCCAGUCUCUUTT 21
      ||:|||||:|:|:|
Db      20 CCTGCCAGTCTCTGT 5

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 08:00:46 ; Search time 2487 Seconds
(without alignments)
344.706 Million cell updates/sec

Title: US-10-738-413-1
Perfect score: 21
Sequence: 1 uaggaccgcgcagucucucut 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 8033812

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Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	62	US-10-738-413-1	Sequence 1, Appl
2	18	85.7	20	54	US-10-424-041-41	Sequence 41, Appl
3	18	85.7	20	54	US-10-424-041-132	Sequence 132, App
4	17	81.0	20	54	US-10-424-041-56	Sequence 56, Appl
5	17	81.0	20	54	US-10-424-041-144	Sequence 144, App
6	14.8	70.5	19	60	US-10-714-333A-239150	Sequence 239150,
7	14.2	67.6	19	60	US-10-714-333A-62335	Sequence 62335, A
8	14.2	67.6	19	60	US-10-714-333A-1045669	Sequence 1045669
9	14.2	67.6	19	60	US-10-714-333A-1492857	Sequence 1492857,
10	13.8	65.7	19	60	US-10-714-333A-113284	Sequence 113284,
11	13.8	65.7	19	60	US-10-714-333A-113286	Sequence 113286,
12	13.8	65.7	21	62	US-10-770-726-7139	Sequence 7139, Ap
13	13.6	64.8	20	2	PCT-US03-37756-12	Sequence 49, Appl
14	13.6	64.8	20	52	US-10-304-082-11	Sequence 11, Appl
15	13.6	64.8	20	52	US-10-304-082-48	Sequence 48, Appl
16	13.6	64.8	21	63	PCT-US04-15645-2129	Sequence 2129, Ap
17	13.6	64.8	21	63	US-10-847-918-2129	Sequence 91, Appl
18	13.4	63.8	19	60	US-10-714-333A-329070	Sequence 329070,
19	13.4	63.8	19	60	US-10-714-333A-329075	Sequence 329075,
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21	13.4	63.8	19	60	US-10-714-333A-1500115	Sequence 1500115,
22	13.4	63.8	19	60	US-10-714-333A-1500139	Sequence 1500139,
23	13.4	63.8	19	60	US-10-714-333A-35790	Sequence 35790, A
24	13.2	62.9	19	60	US-10-714-333A-36093	Sequence 36093, A
25	13.2	62.9	19	60	US-10-714-333A-36186	Sequence 36186, A
26	13.2	62.9	19	60	US-10-714-333A-59186	Sequence 59186, A
27	13.2	62.9	19	60	US-10-714-333A-115298	Sequence 115298,
28	13.2	62.9	19	60	US-10-714-333A-115378	Sequence 115378,
29	13.2	62.9	19	60	US-10-714-333A-115557	Sequence 115557,
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31	13.2	62.9	19	60	US-10-714-333A-612153	Sequence 612153,
32	13.2	62.9	19	60	US-10-714-333A-1207022	Sequence 1207022,
33	13.2	62.9	19	60	US-10-714-333A-1342729	Sequence 1342729,
34	13.2	62.9	19	60	US-10-714-333A-1492844	Sequence 1492844,
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36	13.2	62.9	21	62	US-10-770-726-36006	Sequence 36006, A
37	13.2	62.9	21	62	PCT-US02-25943-16735	Sequence 16735, A
38	13.2	62.9	15	1	PCT-US02-25943-16736	Sequence 16736, A
39	13.2	62.9	15	50	US-10-227-565-16735	Sequence 16735, A
40	13.2	62.9	15	50	US-10-227-565-16736	Sequence 16736, A
41	13.2	62.9	15	53	US-10-367-832A-16735	Sequence 16735, A
42	13	61.9	15	53	US-10-367-832A-16735	Sequence 16735, A
43	13	61.9	15	53	US-10-367-832A-16735	Sequence 16735, A
44	13	61.9	15	53	US-10-367-832A-16735	Sequence 16735, A
45	13	61.9	15	53	US-10-367-832A-16735	Sequence 16735, A

ALIGNMENTS

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RESULT 1
US-10-738-413-1
; Sequence 1, Application US/10738413
; GENERAL INFORMATION:
; APPLICANT: BINETTI, RALPH R.
; TITLE OF INVENTION: ST-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
; FILE REFERENCE: SC66U-US
; CURRENT APPLICATION NUMBER: US/10/738,413
; CURRENT FILING DATE: 2003-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-738-413-1
Query Match 100.0%; Score 21; DB 62; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.2; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 UAGAGCCUGCCAGGUCUCUTT 21
DB 1 UAGAGCCUGCCAGGUCUCUTT 21

RESULT 2
US-10-424-041-132
; Sequence 41, Application US/10424041
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BIOL0005US
; CURRENT APPLICATION NUMBER: US/10/424,041
; CURRENT FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-424-041-41
Query Match 85.7%; Score 18; DB 54; Length 20;
Best Local Similarity 77.8%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 UAGAGCCUGCCAGGUCUC 18
DB 18 TAGAGCTGCGCAGTGTCTC 1

RESULT 3
US-10-424-041-132
; Sequence 132, Application US/10424041
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
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FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 132
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-424-041-132

Query Match 85.7%; Score 18; DB 54; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGACCTGCCAGUCUC 18
DB 3 UAGACCTGCCAGUCUC 20

RESULT 4
US-10-424-041-56/c
Sequence 56, Application US/10424041
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: Kenneth W. Doble
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-10-424-041-56

Query Match 81.0%; Score 17; DB 54; Length 20;
Best Local Similarity 76.5%; Pred. No. 9.4e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGACCTGCCAGUCUC 17
DB 17 TAGGACCTGCCAGTCT 1

RESULT 5
US-10-424-041-144
Sequence 144, Application US/10424041
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: Kenneth W. Doble
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BIOL0005US
CURRENT APPLICATION NUMBER: US/10/424,041
CURRENT FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 144
LENGTH: 20
TYPE: DNA
ORGANISM: M. musculus
FEATURE:
US-10-424-041-144

Query Match 81.0%; Score 17; DB 54; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGACCTGCCAGUCUC 17
DB 4 UAGACCTGCCAGUCUC 20

RESULT 6
US-10-714-333A-239150
Sequence 239150, Application US/10714333A
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 239150
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-10-714-333A-239150

Query Match 70.5%; Score 14.8; DB 60; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.2e+04;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCTGCCAGUCUCUTT 21
DB 2 GACCTGCCAGUCUCUUU 19

RESULT 7
US-10-714-333A-62335
Sequence 62335, Application US/10714333A
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/10/714,333A
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 62335
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-10-714-333A-62335

Query Match 67.6%; Score 14.2; DB 60; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+04;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGACCTGCCAGUCUCUTT 21
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Db 1 GGACCUACGAGGCUCAU 19

RESULT 8

US-10-714-333A-1045669
; Sequence 1045669, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
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; PRIOR APPLICATION NUMBER: 60/426,137
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; SOFTWARE: Proprietary
; SEQ ID NO 1045669
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1045669

Query Match 67.6%; Score 14.2; DB 60; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+04;

Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGACCUACGAGGCUCAU 21
Db 1 GGACCUACGAGGCUCAU 19

Db 1 GGACCUACGAGGCUCAU 19

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; Sequence 1492857, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
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; SEQ ID NO 1492857
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-1492857

Query Match 67.6%; Score 14.2; DB 60; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.4e+04;

Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db 1 GGACCUACGAGGCUCAU 19

Db 1 GGACCUACGAGGCUCAU 19

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; Sequence 113284, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 113284
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-113284

US-10-714-333A-113284

Query Match 65.7%; Score 13.8; DB 60; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.8e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACCUGCCAGUGUCUUT 21
Db 2 ACCUGCCAGUGUCUUT 18

RESULT 11

US-10-714-333A-113286
; Sequence 113286, Application US/10714333A
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333A
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 113286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333A-113286

Query Match 65.7%; Score 13.8; DB 60; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.8e+04;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACCUGCCAGUGUCUUT 21
Db 3 ACCUGCCAGUGUCUUT 19

RESULT 12

US-10-770-726-7139/c
; Sequence 7139, Application US/107070726

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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7139
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10,770-726-7139

Query Match
Best Local Similarity 65.7%; Score 13.8; DB 62; Length 21;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy
2 AGGACCCGCGAGGCTCTT 21
Db
17 AGGACCTGCTGCTGCTT 1

RESULT 13
PCT-US03-37756-12
; Sequence 12, Application PC/TUS0337756
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: ISPT-1008
; CURRENT APPLICATION NUMBER: PCT/US03/37756
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,082
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US03-37756-12

Query Match
Best Local Similarity 64.8%; Score 13.6; DB 2; Length 20;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy
2 AGGACCCGCGAGGCTCTT 21
Db
1 AGGACCTGCTGAGGCTCTT 20

RESULT 14
PCT-US03-37756-49/C
; Sequence 49, Application PC/TUS0337756
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: ISPT-1008
; CURRENT APPLICATION NUMBER: PCT/US03/37756
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,082
; PRIOR FILING DATE: 2002-11-22
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; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37756-49

Query Match
Best Local Similarity 64.8%; Score 13.6; DB 2; Length 20;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy
2 AGGACCCGCGAGGCTCTT 21
Db
20 AGGACCTGCTGAGGCTCTT 1

RESULT 15
US-10-304-082-11
; Sequence 11, Application US/10304082
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF JAGGED 1 EXPRESSION
; FILE REFERENCE: PTS-0037
; CURRENT APPLICATION NUMBER: US/10/304,082
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-082-11

Query Match
Best Local Similarity 64.8%; Score 13.6; DB 52; Length 20;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy
2 AGGACCCGCGAGGCTCTT 21
Db
1 AGGACCTGCTGAGGCTCTT 20
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Search completed: September 17, 2005, 09:49:56
Job time : 2489 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2005, 08:05:35 ; Search time 1261 Seconds

(without alignments)
226.200 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 usagaccgcagcagcucut 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 24829634 seqs, 6791393036 residues 23489972

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Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	2	PCT-US04-39941-1
2	18	85.7	20	21	US-11-071-788-41
3	18	85.7	20	21	US-11-071-788-132
4	17.8	84.8	21	12	US-10-605-923-344173
5	17.8	84.8	21	12	US-10-605-924-682886
6	17.8	84.8	21	16	US-10-310-914A-682886
7	17	81.0	20	21	US-11-071-788-56

8	17	81.0	20	21	US-11-071-788-144	Sequence 144, App
9	16.4	78.1	21	11	US-10-604-985A-21186	Sequence 21186, A
10	15.2	72.4	21	12	US-10-604-985-21186	Sequence 21186, A
11	15.2	72.4	21	12	US-10-605-923-784389	Sequence 784389, A
12	15.2	72.4	21	13	US-10-605-924-964352	Sequence 964352, A
13	15.2	72.4	21	16	US-10-310-914A-964352	Sequence 964352, A
14	14.8	70.5	19	2	PCT-US03-36787-239150	Sequence 239150, A
15	14.8	70.5	19	14	US-10-714-333B-239150	Sequence 239150, A
16	14.8	70.5	19	22	US-11-083-784-239150	Sequence 239150, A
17	14.8	70.5	19	23	US-11-093-832-239150	Sequence 239150, A
18	14.8	70.5	19	25	US-11-101-244-239150	Sequence 239150, A
19	14.6	69.5	21	11	US-10-707-9758-452899	Sequence 452899, A
20	14.6	69.5	21	12	US-10-605-924-193827	Sequence 193827, A
21	14.6	69.5	21	16	US-10-310-914A-193827	Sequence 193827, A
22	14.4	68.6	17	11	US-10-707-9758-145451	Sequence 145451, A
23	14.4	68.6	17	12	US-10-605-923-131526	Sequence 131526, A
24	14.4	68.6	18	13	US-10-605-924-1315887	Sequence 1315887, A
25	14.4	68.6	18	16	US-10-310-914A-1315887	Sequence 1315887, A
26	14.4	68.6	19	13	US-10-605-924-1315888	Sequence 1315888, A
27	14.4	68.6	19	16	US-10-310-914A-1315888	Sequence 1315888, A
28	14.2	67.6	19	2	PCT-US03-36787-62335	Sequence 62335, A
29	14.2	67.6	19	2	PCT-US03-36787-1045669	Sequence 1045669, A
30	14.2	67.6	19	2	PCT-US03-36787-1492857	Sequence 1492857, A
31	14.2	67.6	19	14	US-10-714-333B-62335	Sequence 62335, A
32	14.2	67.6	19	14	US-10-714-333B-1045669	Sequence 1045669, A
33	14.2	67.6	19	14	US-10-714-333B-1492857	Sequence 1492857, A
34	14.2	67.6	19	22	US-11-083-784-62335	Sequence 62335, A
35	14.2	67.6	19	22	US-11-083-784-1045669	Sequence 1045669, A
36	14.2	67.6	19	23	US-11-083-784-1492857	Sequence 1492857, A
37	14.2	67.6	19	23	US-11-093-832-62335	Sequence 62335, A
38	14.2	67.6	19	23	US-11-093-832-1045669	Sequence 1045669, A
39	14.2	67.6	19	23	US-11-093-832-1492857	Sequence 1492857, A
40	14.2	67.6	19	24	US-11-095-383-62335	Sequence 62335, A
41	14.2	67.6	19	25	US-11-101-244-62335	Sequence 62335, A
42	14.2	67.6	19	25	US-11-101-244-1045669	Sequence 1045669, A
43	14.2	67.6	19	25	US-11-101-244-1492857	Sequence 1492857, A
44	14.2	67.6	21	11	US-10-707-9758-500017	Sequence 500017, A
45	14.2	67.6	21	12	US-10-605-923-327282	Sequence 327282, A

ALIGNMENTS

RESULT 1
PCT-US04-39941-1
Sequence 1, Application PC/TUS0439941
GENERAL INFORMATION:
APPLICANT: AVON PRODUCTS, INC.
TITLE OF INVENTION: SI-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
FILE REFERENCE: TYROSINASE AND REDUCE PIGMENTATION
CURRENT FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: 10/738,413
PRIOR FILING DATE: 2003-12-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
PCT-US04-39941-1
Query Match 100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      1
      Qy      1 UAGACCGCCAGUGCUCU 21
              |||||
      Db      1 UAGACCGCCAGUGCUCU 21

RESULT 2
US-11-071-788-41/c
; Sequence 41, Application US/11071788
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: James Karras
; APPLICANT: Susan Filch
; APPLICANT: Ravi Jain
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BNDL-001705.P1
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: US 10/424,041
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/704,263
; PRIOR FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 10/889,101
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US 60/486,652
; PRIOR FILING DATE: 2003-07-12
; PRIOR APPLICATION NUMBER: US 10/889,447
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US 60/486,670
; PRIOR FILING DATE: 2003-07-12
; PRIOR APPLICATION NUMBER: US 10/498,704
; PRIOR FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: PCT/US02/39873
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 10/029,517
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 184
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-11-071-788-41

Query Match      85.7%; Score 18; DB 21; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 UAGACCGCCAGUGCUC 18
      :|||||:|||||:|
Db      18 TAGACCTGCGAGTGTCTC 1

RESULT 3
US-11-071-788-132
; Sequence 132, Application US/11071788
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Thomas Condon
; APPLICANT: Susan M. Freier
; APPLICANT: James Karras
; APPLICANT: Susan Filch
; APPLICANT: Ravi Jain
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
; FILE REFERENCE: BNDL-001705.P1
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: US 10/424,041
; PRIOR FILING DATE: 2003-04-25
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      1
      Qy      1 UAGACCGCCAGUGCUC 18
              |||||
      Db      3 UAGACCGCCAGUGCUC 20

RESULT 4
US-10-605-923-344173
; Sequence 344173, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 344173
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-344173

Query Match      84.8%; Score 17.8; DB 12; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      1 UAGACCGCCAGUGCUCU 21
      :|||||:|||||:|
Db      1 TGGACCTGCCAGTGTCTGT 21

RESULT 5
US-10-605-924-682886/c
; Sequence 682886, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 682886
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LENGTH: 21
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-605-924-682886

Query Match 84.8%; Score 17.8; DB 12; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGACCGCCAGUCGUCCTT 21
DB 21 TGGGACCTGCGAGTCTCTGT 1

RESULT 6
US-10-310-914A-682886/c
Sequence 682886, Application US/10310914A
GENERAL INFORMATION:
APPLICANT: Benitwich, Isaac

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 682886
LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-310-914A-682886

Query Match 84.8%; Score 17.8; DB 16; Length 21;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 14; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGACCGCCAGUCGUCCTT 21
DB 21 TGGGACCTGCGAGTCTCTGT 1

RESULT 7
US-11-071-788-56/c
Sequence 56, Application US/11071788
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: James Karras
APPLICANT: Susan Fitch
APPLICANT: Ravi Jain
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BNDL-0017US.P1
CURRENT APPLICATION NUMBER: US/11/071,788
PRIOR FILING DATE: 2005-03-02
PRIOR APPLICATION NUMBER: US 10/424,041
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 10/704,263
PRIOR FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: US 10/889,101
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,652
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/889,447
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,670
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/498,704
PRIOR FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: PCT/US02/39873
PRIOR FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: US 10/029,517
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Antisense Oligonucleotide
US-11-071-788-56

Query Match 81.0%; Score 17; DB 21; Length 20;
Best Local Similarity 76.5%; Pred. No. 3.6e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGACCGCCAGUCGCU 17
DB 17 TAGGACCTGCGAGTCT 1

RESULT 8
US-11-071-788-144
Sequence 144, Application US/11071788
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Thomas Condon
APPLICANT: Susan M. Freiler
APPLICANT: James Karras
APPLICANT: Susan Fitch
APPLICANT: Ravi Jain
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF TYROSINASE EXPRESSION
FILE REFERENCE: BNDL-0017US.P1
CURRENT APPLICATION NUMBER: US/11/071,788
PRIOR FILING DATE: 2005-03-02
PRIOR APPLICATION NUMBER: US 10/424,041
PRIOR FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 10/704,263
PRIOR FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: US 10/889,101
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,652
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/889,447
PRIOR FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US 60/486,670
PRIOR FILING DATE: 2003-07-12
PRIOR APPLICATION NUMBER: US 10/498,704
PRIOR FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: PCT/US02/39873
PRIOR FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 10/029,517
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 184
SEQ ID NO 144
LENGTH: 20
TYPE: DNA
ORGANISM: M. musculus
FEATURE:

US-11-071-788-144

Query Match 81.0%; Score 17; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAGACCGCCAGUCGCU 17
DB 4 UAGACCGCCAGUCGCU 20

RESULT 9
US-10-604-985A-21186
Sequence 21186, Application US/10604985A

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; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55011
; CURRENT APPLICATION NUMBER: US/10/604,985A
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 97967
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21186
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Human
US-10-604-985A-21186
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Query Match      78.1%; Score 16.4; DB 11; Length 21;
Best Local Similarity 72.2%; Pred. No. 7.3e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 UAGGACCGCCAGGCGCUC 18
      : |||||: |||||: |||||:
Db      4 TGGGACCTGCCAGTGTCTC 21
```

```
RESULT 10
US-10-604-985-21186
; Sequence 21186, Application US/10604985
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55011
; CURRENT APPLICATION NUMBER: US/10/604,985
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 97947
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21186
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-604-985-21186
```

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Query Match      78.1%; Score 16.4; DB 12; Length 21;
Best Local Similarity 72.2%; Pred. No. 7.3e+02;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 UAGGACCGCCAGGCGCUC 18
      : |||||: |||||: |||||:
Db      4 TGGGACCTGCCAGTGTCTC 21
```

```
RESULT 11
US-10-605-923-784389/C
; Sequence 784389, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 784389
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-784389
```

```
Query Match      72.4%; Score 15.2; DB 12; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 UAGGACCGCCAGGCGCUC 20
      : |||||: |||||: |||||:
Db      21 TAGGATCTCCAGTGTCTCTT 2
```

```
RESULT 12
US-10-605-924-964352
; Sequence 964352, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 964352
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-964352
```

```
Query Match      72.4%; Score 15.2; DB 13; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 UAGGACCGCCAGGCGCUC 20
      : |||||: |||||: |||||:
Db      1 TAGGATCTCCAGTGTCTCTT 20
```

```
RESULT 13
US-10-310-914A-964352
; Sequence 964352, Application US/10310914A
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Krzysztof
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 964352
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-964352
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```
Query Match      72.4%; Score 15.2; DB 16; Length 21;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 UAGGACCGCCAGGCGCUC 20
      : |||||: |||||: |||||:
Db      1 UAGGACCGCCAGGCGCUCU 20
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RESULT 14
PCT-US03-36787-239150
; Sequence 239150, Application PC/TUS0336787
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leahe, Devin
; APPLICANT: Marshall, William
; APPLICANT: Read, Steven
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Methods and Compositions for Improving
; TITLE OF INVENTION: siRNA functionality
```



```

; FILE REFERENCE: 1349PCT
; CURRENT APPLICATION NUMBER: PCT/US03/36787
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 239150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US03-36787-239150

```

```

Query Match 70.5%; Score 14.8; DB 2; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 4 GACCGCCGAGUCUCUUTT 21
Db 2 GACCGCCGAGUCUCUUTT 19

```

```

RESULT 15
US-10-714-333B-239150
; Sequence 239150, Application US/10714333B
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/10/714,333B
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 239150
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-714-333B-239150

```

```

Query Match 70.5%; Score 14.8; DB 14; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.6e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GACCGCCGAGUCUCUUTT 21
Db 2 GACCGCCGAGUCUCUUTT 19

```

Search completed: September 17, 2005, 10:11:06
Job time : 1264 secs

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